

Automatic sample mounting and alignment system for macromolecular crystallography at the ALS

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ABSTRACT

In an effort to realize high-throughput, automated data collection for macromolecular crystallography, we have developed and installed an automatic cryogenic sample mounting and alignment system for protein crystals. This system has been installed on BCSB/ALS beamline 5.0.3 at the Advanced Light Source. The automounter was installed and began testing in March of 2001 and has been in user operation since September, 2001 with reliable performance. To further increase throughput, we have also developed a sample transport/storage system based on "puck-shaped" cassettes which can hold 16 samples each. Centering of a crystal can be done by the user through the remote controlled xyz goniometer head or automatically by a centering algorithm. Our near term goal is to achieve fully automated screening (i.e. mounting, centering and exposing) of all samples in the dewar (currently 64) and to increase the capacity of the automounter dewar. Compatibility with systems available at other beamlines and facilities is a necessary design criteria. Software for the advanced control of these experiments is also under development.

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